AMENDMENTS

In the specification:

Please replace the paragraph beginning on line page 47, line 5 with the following rewritten paragraph:

The alignment of GFP-like proteins (see supplemental data) was constructed after Matz, M. V., Fradkov, A. F., Labas, Y. A., Savitsky, A. P., Zaraisky, A. G., Markelov, M. L. & Lukyanov, S. A. (1999) *Nat Biotechnol* 17, 969-73 taking in account constraints of the protein structure. Then the DNA alignment was made following the protein alignment; excluding the poorly aligned N- and C-terminal regions. The phylogenetic tree was constructed using Tree-Puzzle software (Strimmer, K. & von Haeseler, A. (1996) *Mol. Biol. Evol.* 13, 964-969) under HKY model of DNA evolution (Hasegawa, M., Kishino, H. & Yano, K. (1985) *J. Mol. Evol.* 22, 160-174), assuming that the variability of sites follows gamma-distribution with alpha parameter estimated from the dataset. The tree was confirmed to be the maximum likelihood tree by PAML software (Yang, Z. (2000) (University College (available on the worldwide web at abacus**(dot)[[.]]**gene**(dot)[[.]]**ucl**(dot)[[.]]**ac**(dot)[[.]]**uk/software/paml**(dot)[[.]]**html), London, England)) under REV model (Yang, Z. H., Goldman, N. & Friday, A. (1994) *Molecular Biology and Evolution* 11, 316-324). The tree built by Tree-Puzzle from protein alignment (JTT model, (Jones, D. T., Taylor, W. R. & Thornton, J. M. (1992) *CABIOS* 8, 275-282) had the same topology but lower support values due to smaller number of informative sites in the protein alignment.